```
            1                                                    50
PmCS        MNTLSQAIKA YNSNDYELAL KLFEKSAETY GRKIVEFQII KCKEKLSTNS
PmHAS       MNTLSQAIKA YNSNDYQLAL KLFEKSAEIY GRKIVEFQIT KCKEKLSAHP
Consensus   MNTLSQAIKA YNSNDY#LAL KLFEKSAEiY GRKIVEFQIi KCKEKLSanp

            51                                                   100
PmCS        YVS....... EDKKNSVCDS SLDIATQLLL SNVKKLTLSE SEKNSLKNKW
PmHAS       SVNSAHLSVN KEEKVNVCDS PLDIATQLLL SNVKKLVLSD SEKNTLKNKW
Consensus   sVn....... e#eKnnVCDS pLDIATQLLL SNVKKLtLS# SEKNsLKNKW

            101                                                  150
PmCS        KSITGKKSEN AEIRKVELVP KDFPKDLVLA PLPDHVNDFT WYKNRKKSLG
PmHAS       KLLTEKKSEN AEVRAVALVP KDFPKDLVLA PLPDHVNDFT WYKKRKKRLG
Consensus   KliTeKKSEN AE!RaVaLVP KDFPKDLVLA PLPDHVNDFT WYKnRKKrLG

            151                                                  200
PmCS        IKPVNKNIGL SIIIPTFNRS RILDITLACL VNQKTNYPFE VVVADDGSKE
PmHAS       IKPEHQHVGL SIIVTTFNRP AILSITLACL VNQKTHYPFE VIVTDDGSQE
Consensus   IKPenqn!GL SII!pTFNRp aILdITLACL VNQKTnYPFE V!VaDDGSqE

            201                                                  250
PmCS        NLLTIVQKYE QKLDIKYVRQ KDYGYQLCAV RNLGLRTAKY DFVSILDCDM
PmHAS       DLSPIIRQYE NKLDIRYVRQ KDNGFQASAA RNMGLRLAKY DFIGLLDCDM
Consensus   #LlpI!rqYE #KLDIrYVRQ KDnG%QacAa RN$GLRlAKY DF!giLDCDM
```

Fig. 1a

```
            251                                                        300
PmCS        APQQLWVHSY LTELLEDNDI VLIGPRKYVD THNITAEQFL NDPYLIESLP
PmHAS       APNPLWVHSY VAELLEDDDL TIIGPRKYID TQHIDPKDFL NNASLLESLP
Consensus   AP#qLWVHSY laELLED#Di tiIGPRKY!D TqnIdae#FL N#asLiESLP

            301                                                        350
PmCS        ETATNNNPSI TSKGNISLDW RLEHFKKTDN LRLCDSPFRY FSCGNVAFSK
PmHAS       EVKTNNSVAA KGEGTVSLDW RLEQFEKTEN LRLSDSPFRF FAAGNVAFAK
Consensus   EtaTNNnpaa kgeGn!SLDW RLEqFeKT#N LRLcDSPFR% FaaGNVAFaK

            351                                                        400
PmCS        EWLNKVGWFD EEFNHWGGED VEFGYRLFAK GCFFRVIDGG MAYHQEPPGK
PmHAS       KWLNKSGFFD EEFNHWGGED VEFGYRLFRY GSFFKTIDGI MAYHQEPPGK
Consensus   eWLNKsGfFD EEFNHWGGED VEFGYRLFak GcFFrtIDGg MAYHQEPPGK

            401                                                        450
PmCS        ENETDREAGK SITLKIVKEK VPYIYRKLLP IEDSHIHRIP LVSIYIPAYN
PmHAS       ENETDREAGK NITLDIMREK VPYIYRKLLP IEDSHINRVP LVSIYIPAYN
Consensus   ENETDREAGK nITLdImrEK VPYIYRKLLP IEDSHInR!P LVSIYIPAYN

            451                                                        500
PmCS        CANYIQRCVD SALNQTVVDL EVCICNDGST DNTLEVINKL YGNNPRVRIM
PmHAS       CANYIQRCVD SALNQTVVDL EVCICNDGST DNTLEVINKL YGNNPRVRIM
Consensus   CANYIQRCVD SALNQTVVDL EVCICNDGST DNTLEVINKL YGNNPRVRIM
```

Fig. 1b

```
           501                                                        550
PmCS       SKPNGGIASA SNAAVSFAKG YYIGQLDSDD YLEPDAVELC LKEFLKDKTL
PmHAS      SKPNGGIASA SNAAVSFAKG YYIGQLDSDD YLEPDAVELC LKEFLKDKTL
Consensus  SKPNGGIASA SNAAVSFAKG YYIGQLDSDD YLEPDAVELC LKEFLKDKTL

           551                                                        600
PmCS       ACVYTTNRNV NPDGSLIANG YNWPEFSREK LTTAMIAHHF RMFTIRAWHL
PmHAS      ACVYTTNRNV NPDGSLIANG YNWPEFSREK LTTAMIAHHF RMFTIRAWHL
Consensus  ACVYTTNRNV NPDGSLIANG YNWPEFSREK LTTAMIAHHF RMFTIRAWHL

           601                                                        650
PmCS       TDGFNENIEN AVDYDMFLKL SEVGKFKHLN KICYNRVLHG DNTSIKKLGI
PmHAS      TDGFNEKIEN AVDYDMFLKL SEVGKFKHLN KICYNRVLHG DNTSIKKLGI
Consensus  TDGFNEnIEN AVDYDMFLKL SEVGKFKHLN KICYNRVLHG DNTSIKKLGI

           651                                                        700
PmCS       QKKNHFVVVN QSLNRQGINY YNYDKFDDLD ESRKYIFNKT AEYQEEMDIL
PmHAS      QKKNHFVVVN QSLNRQGITY YNYDEFDDLD ESRKYIFNKT AEYQEEIDIL
Consensus  QKKNHFVVVN QSLNRQGInY YNYDeFDDLD ESRKYIFNKT AEYQEEiDIL

           701                                                        750
PmCS       KDLKLIQNKD AKIAVSIFYP NTLNGLVKKL NNIIEYNKNI FVIILHVDKN
PmHAS      KDIKIIQNKD AKIAVSIFYP NTLNGLVKKL NNIIEYNKNI FVIVLHVDKN
Consensus  KDiKiIQNKD AKIAVSIFYP NTLNGLVKKL NNIIEYNKNI FVI!LHVDKN
```

Fig. 1c

```
            751                                                        800
PmCS        HLTPDIKKEI LAFYHKHQVN ILLNNDISYY TSNRLIKTEA HLSNINKLSQ
PmHAS       HLTPDIKKEI LAFYHKHQVN ILLNNDISYY TSNRLIKTEA HLSNINKLSQ
Consensus   HLTPDIKKEI LAFYHKHQVN ILLNNDISYY TSNRLIKTEA HLSNINKLSQ

            801                                                        850
PmCS        LNLNCEYIIF DNHDSLFVKN DSYAYMKKYD VGMNFSALTH DWIEKINAHP
PmHAS       LNLNCEYIIF DNHDSLFVKN DSYAYMKKYD VGMNFSALTH DWIEKINAHP
Consensus   LNLNCEYIIF DNHDSLFVKN DSYAYMKKYD VGMNFSALTH DWIEKINAHP

            851                                                        900
PmCS        PFKKLIKTYF NDNDLRSMNV KGASQGMFMK YALPHELLTI IKEVITSCQS
PmHAS       PFKKLIKTYF NDNDLKSMNV KGASQGMFMT YALAHELLTI IKEVITSCQS
Consensus   PFKKLIKTYF NDNDLrSMNV KGASQGMFMk YALaHELLTI IKEVITSCQS

            901                                                        950
PmCS        IDSVPEYNTE DIWFQFALLI LEKKTGHVFN KTSTLTYMPW ERKLQWTNEQ
PmHAS       IDSVPEYNTE DIWFQFALLI LEKKTGHVFN KTSTLTYMPW ERKLQWTNEQ
Consensus   IDSVPEYNTE DIWFQFALLI LEKKTGHVFN KTSTLTYMPW ERKLQWTNEQ

            951                  972
PmCS        IQSAKKGENI PVNKFIINSI TL
PmHAS       IESAKRGENI PVNKFIINSI TL
Consensus   I#SAKrGENI PVNKFIINSI TL
```

Fig. 1d

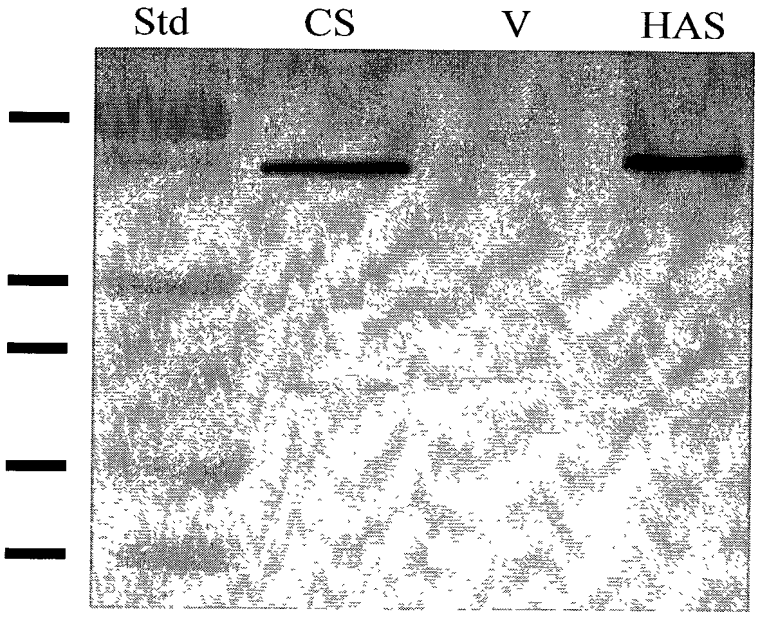


Fig. 2

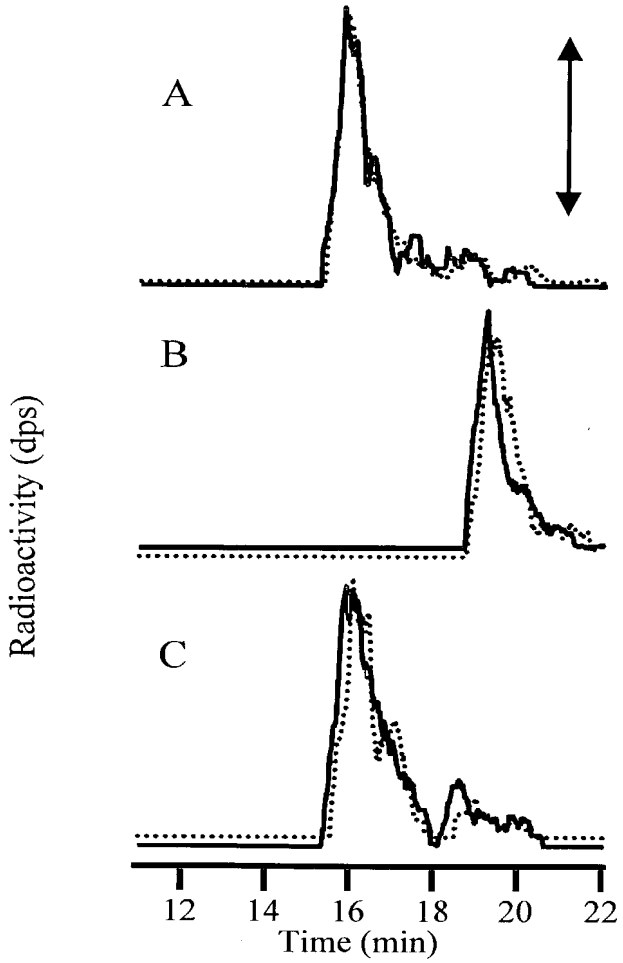


Fig. 3

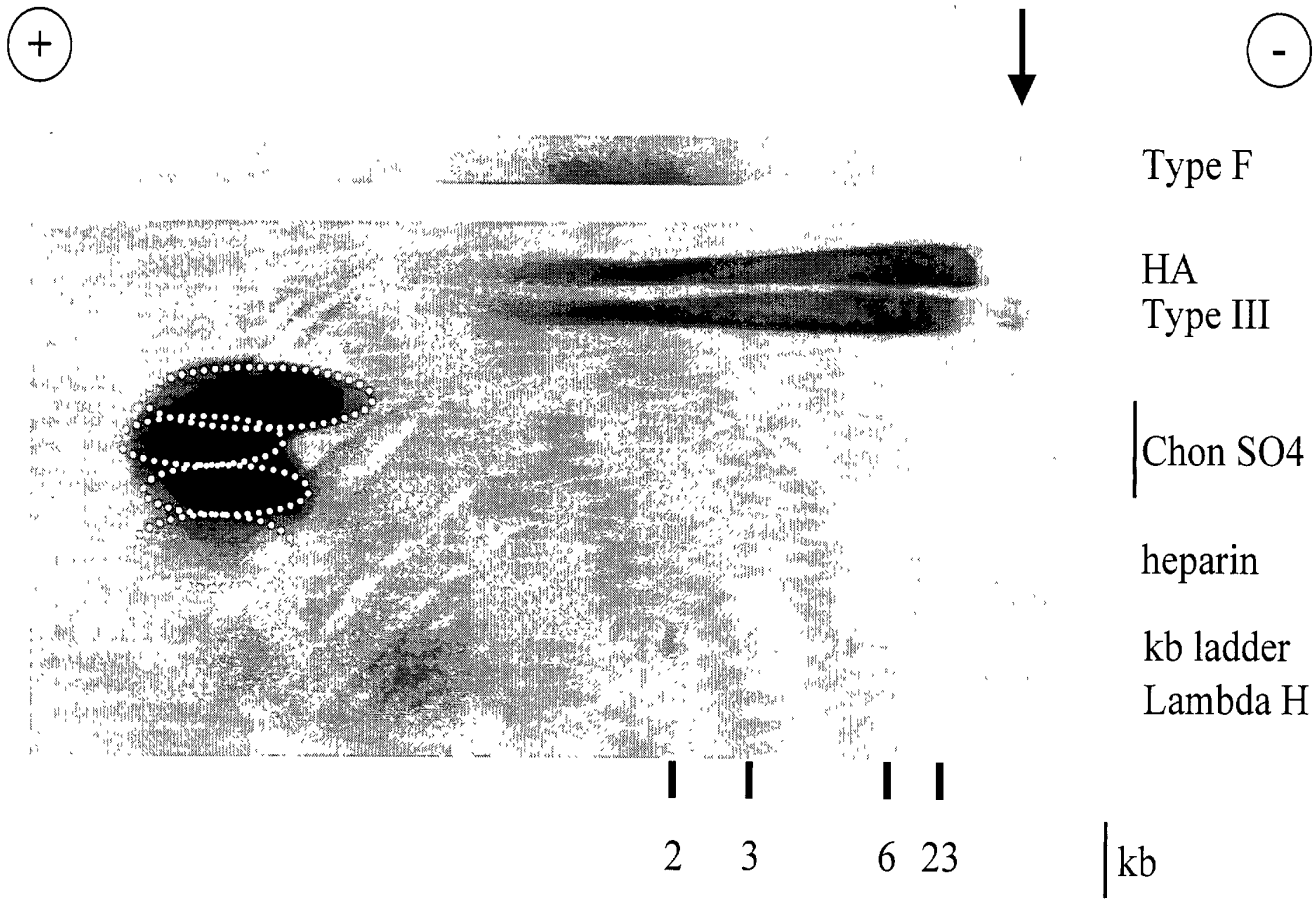
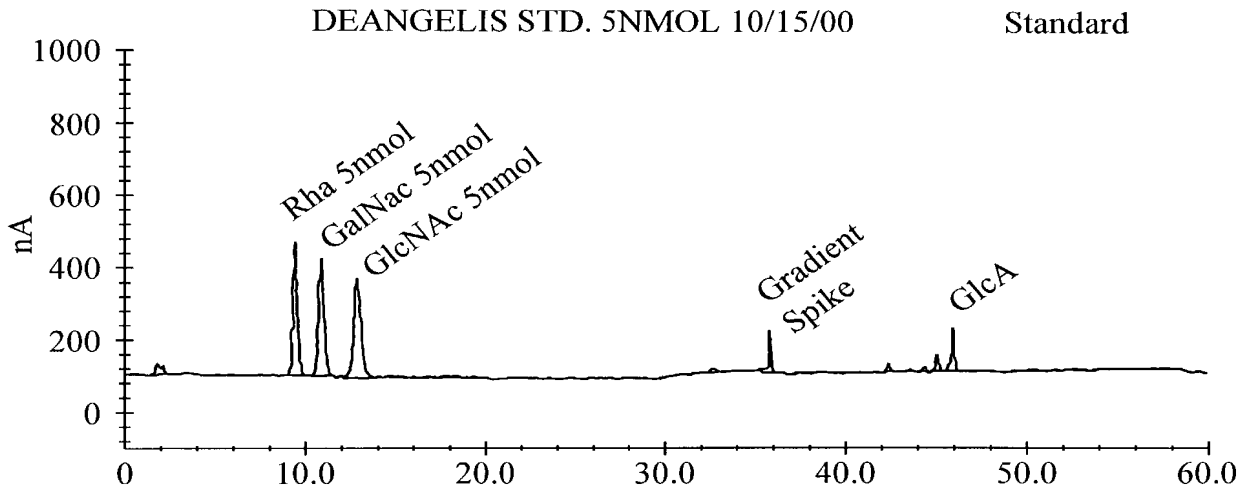

+
-
Type F
HA
Type III
Chon SO4
heparin
kb ladder
Lambda H
2
3
6
23
kb

Fig. 4


DEANGELIS STD. 5NMOL 10/15/00
Standard
1000
800
600
400
200
0
nA
Rha 5nmol
GalNac 5nmol
GlcNAc 5nmol
Gradient
Spike
GlcA
0
10.0
20.0
30.0
40.0
50.0
60.0

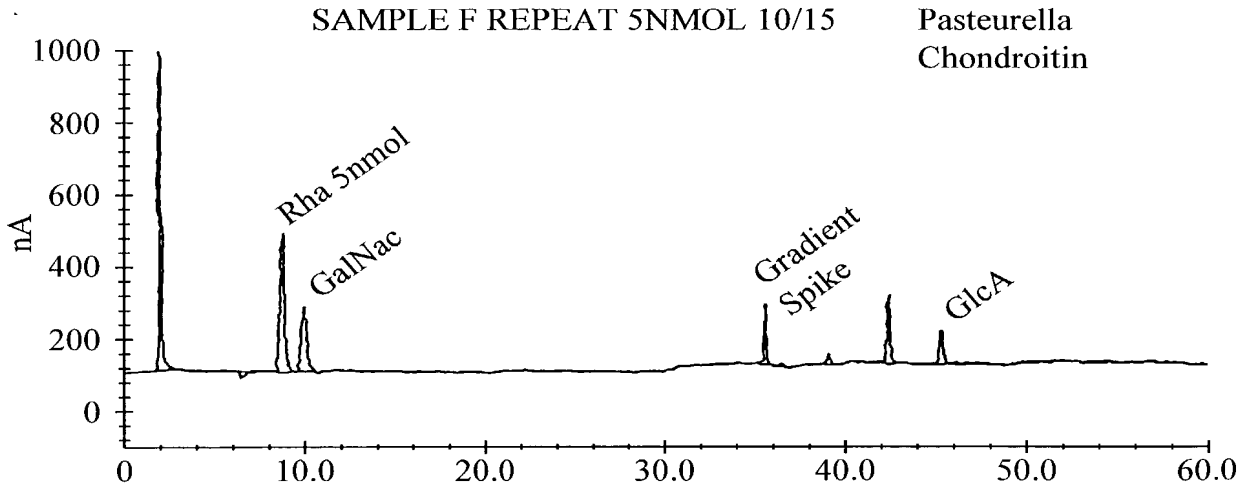

SAMPLE F REPEAT 5NMOL 10/15
Pasteurella
Chondroitin
1000
800
600
400
200
0
nA
Rha 5nmol
GalNac
Gradient
Spike
GlcA
0
10.0
20.0
30.0
40.0
50.0
60.0

Fig. 5

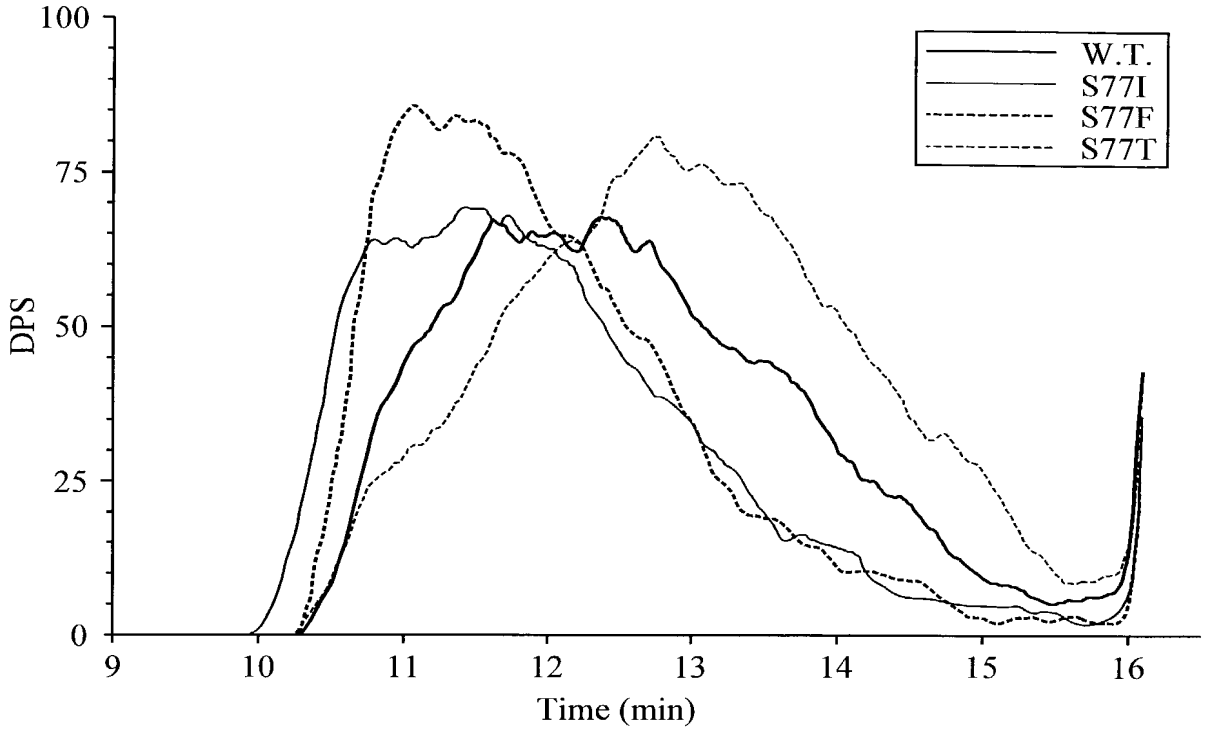

100
75
50
25
0
DPS
9
10
11
12
13
14
15
16
Time (min)
W.T.
S77I
S77F
S77T

Fig. 6

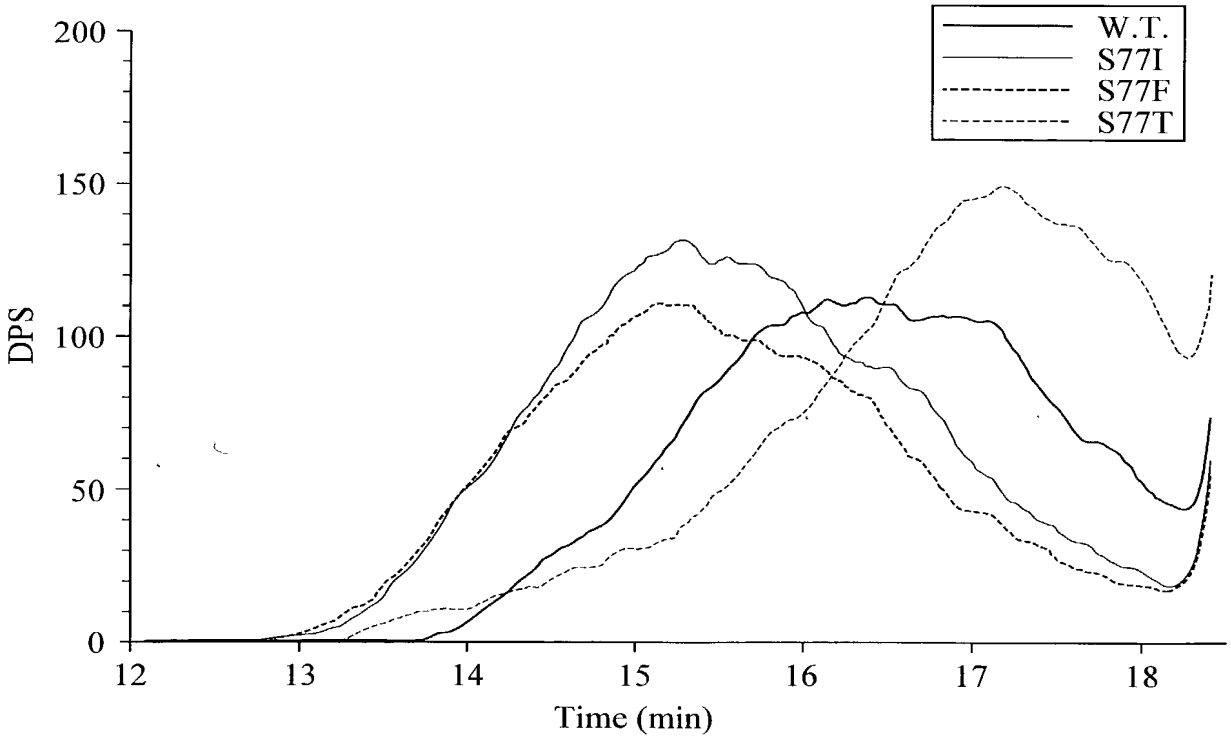

200
150
100
50
0
DPS
12
13
14
15
16
17
18
Time (min)
W.T.
S77I
S77F
S77T

Fig. 7

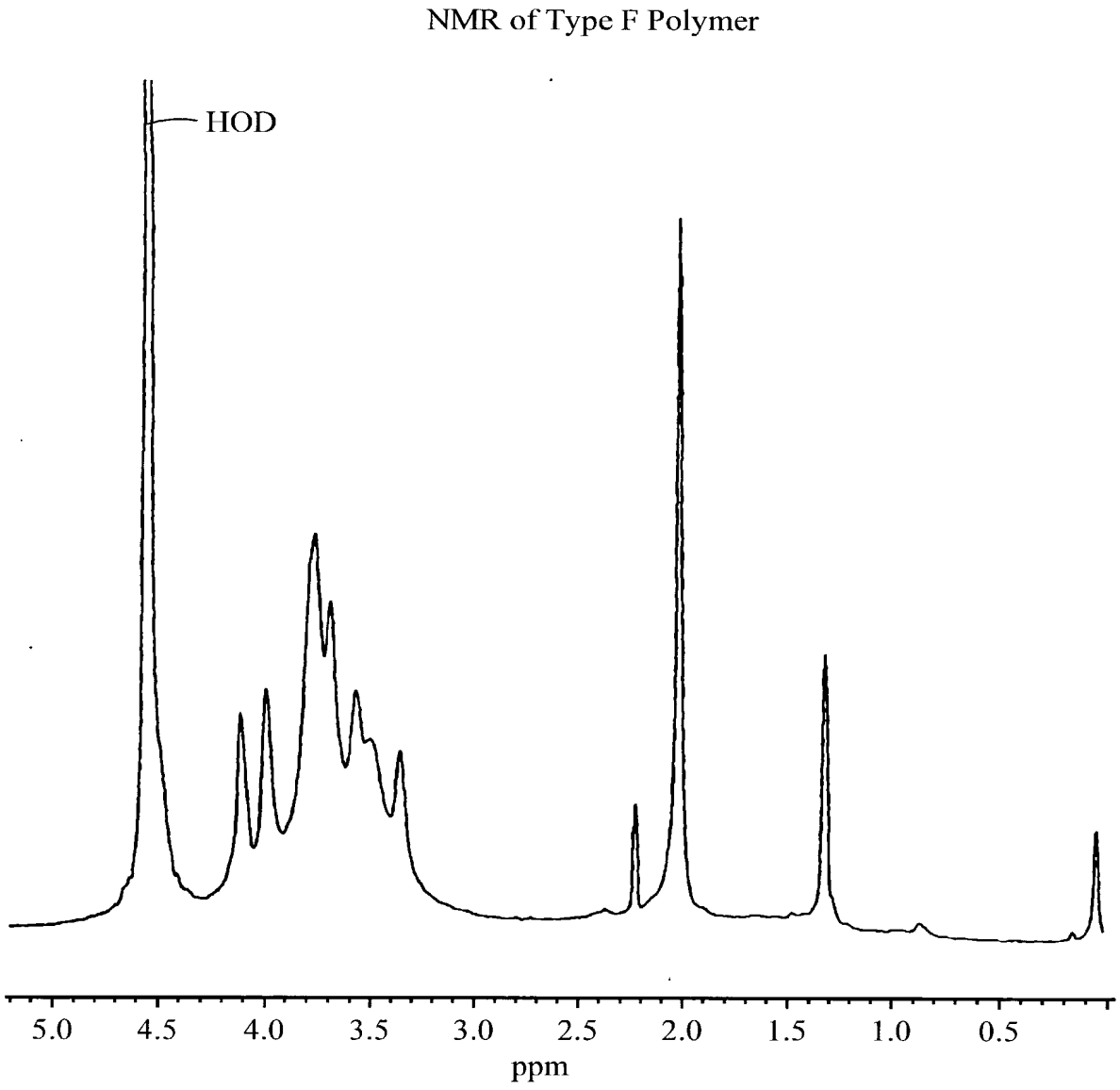


Fig. 8

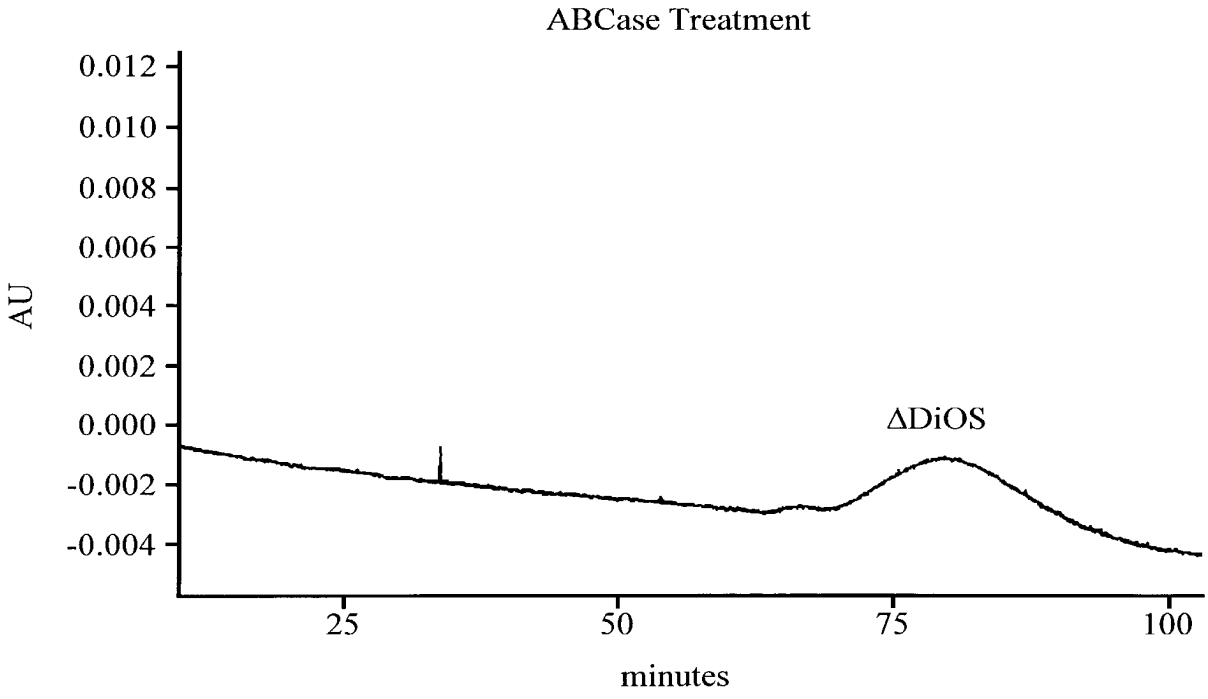

ABCase Treatment
0.012
0.010
0.008
0.006
0.004
0.002
0.000
-0.002
-0.004
AU
ΔDiOS
25
50
75
100
minutes

Fig. 9

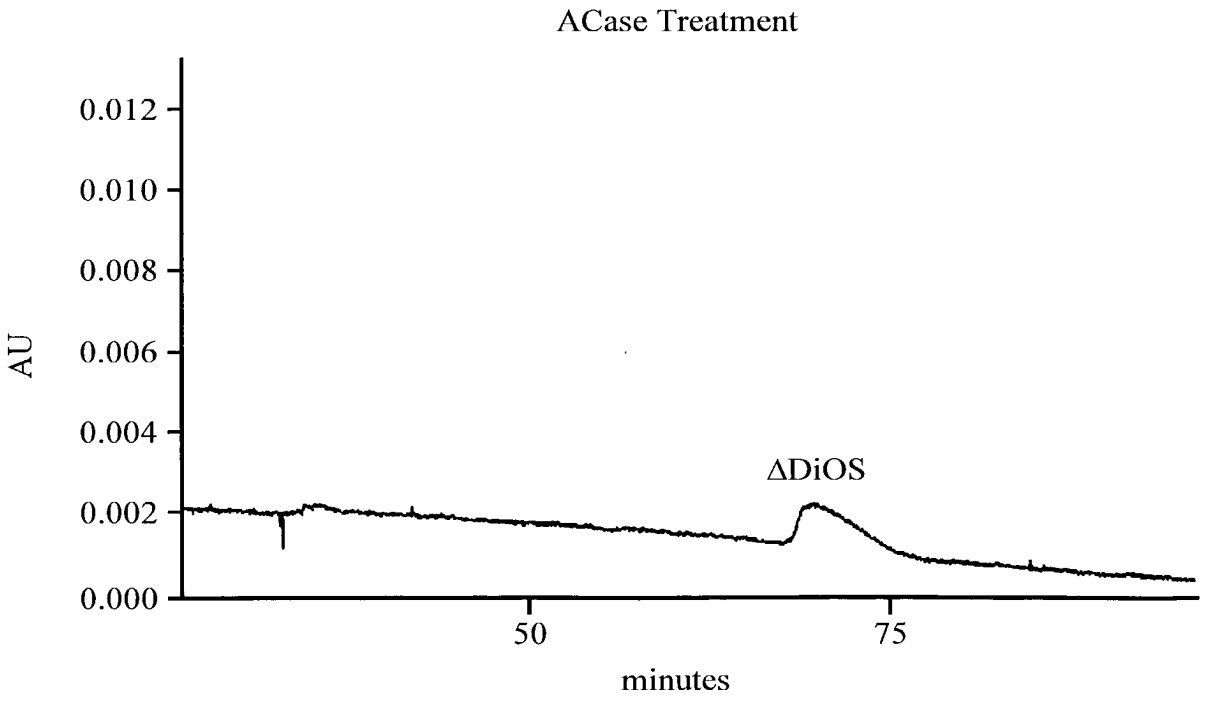

ACase Treatment
0.012
0.010
0.008
0.006
0.004
0.002
0.000
AU
ΔDiOS
50
75
minutes

Fig. 10